



What is claimed is:

Sub1317

- 1. A method for discriminating among members of one or more taxonomic groups by hybridization analysis of operan subsequences either as DNA or as the RNA product(s) comprising the steps of:
- a. determining operon subsequence reactivity by testing samples with each oligonucleotide probe under controlled stringency conditions at two or more temperatures relative to the probe's calculated or experimentally determined $T_{\rm m}$ or by other changes,
- b. contacting individually one or more samples that may contain operon subsequences with one or more oligonucleotide probes,
- c. incubating the probes and samples at various temperatures and other conditions such that increasing degrees of stringency are obtained,
- d. assaying for hybridization of the probes to the samples in order to determine the relative level of reactivity of the combination of operon subsequences present in each sample.

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2. The method of claim 1 for discriminating among the genera Shigella and Escherichia and their

SEQID NOI a species wherein probe Seq. ID: Number I has the sequence CAG CTT GCT CTT CGC TGA CG.

3. The method of claim 1 for discriminating among the genera Shigella and Escherichia and their

a species wherein probe Seq. ID: Number 2 has the sequence AAA GCA GCT TGC TCT TTG CT

4. The method of claim 1 for discriminating among the genera Shigella and Escherichia and their

SEQ ID NO3

a species wherein probe Seq. ID: Number 3 has the sequence CGA CGC AAC GCG AAG AAC TT.

5. The method of claim 1 for discriminating among the genera Shigella and Escherichia wherein

a probe Seq. ID: NO4 probe Seq. ID: Number 4 has the sequence GAA GCT TGC TTC TTT GCT GAC.

SEQ ID NOS 1,2,3,0,4

6. RNA sequences for probe Seq. ID: Numbers 1, 2, 3, or 4 wherein U substitutes for T.

SEQ ID NOs 1,2,30 7. Variants through addition, subtraction, and/or modification of bases of probe Seq. ID: Number 1,

Q -2; 3, or 4.

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